

#26

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/856,617 D
Source: 1600
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DATE: 10/26/2004

PATENT APPLICATION: US/09/856,617D

TIME: 08:36:53

Input Set : A:\766.52.txt

Output Set: N:\CRF4\10252004\I856617D.raw

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3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.,
5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDE
7 <130> FILE REFERENCE: 766.52
9 <140> CURRENT APPLICATION NUMBER: US 09/856,617D
10 <141> CURRENT FILING DATE: 2001-05-24
12 <150> PRIOR APPLICATION NUMBER: H10-332484
13 <151> PRIOR FILING DATE: 1998-11-24
15 <150> PRIOR APPLICATION NUMBER: H11-248442
16 <151> PRIOR FILING DATE: 1999-09-02
18 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4173
23 <212> TYPE: DNA
24 <213> ORGANISM: Mouse
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (107)..(4021)
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33 tcgggccccg gaacgagccg cgctggcggc ggcggcggtg gccgcg atg atg gag 115
34                                     Met Met Glu
35                                     1
37 atc cag atg gac gag gga gga ggt gtg gtg gtg tac caa gac gac tac 163
38 ile gln met asp glu gly gly gly val val val tyr gln asp asp tyr
39      5              10              15
41 tgc tcg ggc tcg gtc atg tcg gag cgt gtg tcg ggc ctg gcg ggc tcc 211
42 cys ser gly ser val met ser glu arg val ser gly leu ala gly ser
43 20              25              30              35
45 atc tac cgc gag ttc gag cgc ctc att cac tgc tat gac gag gag gtg 259
46 ile tyr arg glu phe glu arg leu ile his cys tyr asp glu glu val
47      40              45              50
49 gtc aag gag ctc atg ccg ctg gtg gtg aac gtg ctg gag aac ctt gac 307
50 val lys glu leu met pro leu val val asn val leu glu asn leu asp
51      55              60              65
53 tcg gtg ctg agc gag aac cag gag cac gag gtg gag ctg gag ctc cta 355
54 ser val leu ser glu asn gln glu his glu val glu leu glu leu leu
55      70              75              80
57 cgc gag gac aac gag cag ctg ctc acg caa tac gag cgc gag aag gcg 403
58 arg glu asp asn glu gln leu leu thr gln tyr glu arg glu lys ala
59      85              90              95
61 ctg cgc aaa cag gcc gag gag aaa ttc atc gaa ttt gaa gat gcc ttg 451
62 leu arg lys gln ala glu glu lys phe ile glu phe glu asp ala leu

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63	100		105		110		115	
65	gaa	caa	gag	aag	aaa	gaa	ctc	cag
66	Glu	Gln	Glu	Lys	Lys	Glu	Leu	Gln
67								
69	cag	aca	cgc	cag	ctg	gag	cta	aag
70	Gln	Thr	Arg	Gln	Leu	Glu	Leu	Lys
71								
73	tcc	cga	ctg	gag	gaa	cga	gaa	tcg
74	Ser	Arg	Leu	Glu	Glu	Arg	Glu	Ser
75								
77	ctg	cac	cag	cgg	cac	aca	gag	atg
78	Leu	His	Gln	Arg	His	Thr	Glu	Met
79								
81	gaa	aga	tcc	aag	atg	cag	caa	gtt
82	Glu	Arg	Ser	Lys	Met	Gln	Gln	Val
83	180							
85	agc	ctg	ccc	ggg	cgg	agg	aag	gag
86	Ser	Leu	Pro	Gly	Arg	Arg	Lys	Glu
87								
89	ccc	ctg	gct	gat	ggc	atg	tgt	cca
90	Pro	Leu	Ala	Asp	Gly	Met	Cys	Pro
91								
93	cag	tcc	tca	gca	gct	gca	aca	ccc
94	Gln	Ser	Ser	Ala	Ala	Ala	Thr	Pro
95								
97	aca	ccc	acg	tcc	tcc	gtg	ccc	tca
98	Thr	Pro	Thr	Ser	Ser	Val	Pro	Ser
99								
101	agc	cta	cag	ccc	ctg	ggg	gac	tat
102	Ser	Leu	Gln	Pro	Leu	Gly	Asp	Tyr
103	260							
105	cag	gcc	cga	gag	aag	cgc	aat	agc
106	Gln	Ala	Arg	Glu	Lys	Arg	Asn	Ser
107								
109	caa	gag	atg	cgg	aac	gtc	agt	atc
110	Gln	Glu	Met	Arg	Asn	Val	Ser	Ile
111								
113	tcc	gat	gtt	cag	gac	att	atc	gac
114	Ser	Asp	Val	Gln	Asp	Ile	Ile	Asp
115								
117	cct	gaa	acc	cgt	ctg	gag	cgc	aca
118	Pro	Glu	Thr	Arg	Leu	Glu	Arg	Thr
119								
121	gta	aac	aaa	gct	ttt	gga	atc	aac
122	Val	Asn	Lys	Ala	Phe	Gly	Ile	Asn
123	340							
125	tcc	acg	gcg	gga	tct	gag	gtc	atc
126	Ser	Thr	Ala	Gly	Ser	Glu	Val	Ile
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130	Leu	Leu	Gly	Glu	Phe	Ser	Val	Arg	Asp	Asp	Phe	Phe	Gly	Met	Gly	Lys	
131			375						380					385			
133	gaa	gtg	ggg	aac	ctg	ctg	ctg	gag	aac	tca	cag	ctt	cta	gag	aca	aaa	1315
134	Glu	Val	Gly	Asn	Leu	Leu	Leu	Glu	Asn	Ser	Gln	Leu	Leu	Glu	Thr	Lys	
135			390						395					400			
137	aat	gct	tta	aat	gta	gtg	aag	aat	gac	ctc	att	gct	aag	gtt	gac	caa	1363
138	Asn	Ala	Leu	Asn	Val	Val	Lys	Asn	Asp	Leu	Ile	Ala	Lys	Val	Asp	Gln	
139		405					410					415					
141	ctg	tca	gga	gaa	cag	gag	gtc	ctg	aag	ggg	gag	ctg	gaa	gca	gcc	aag	1411
142	Leu	Ser	Gly	Glu	Gln	Glu	Val	Leu	Lys	Gly	Glu	Leu	Glu	Ala	Ala	Lys	
143	420						425					430				435	
145	caa	gcg	aaa	gtc	aag	ctg	gag	aac	cga	atc	aaa	gag	ctt	gaa	gaa	gaa	1459
146	Gln	Ala	Lys	Val	Lys	Leu	Glu	Asn	Arg	Ile	Lys	Glu	Leu	Glu	Glu	Glu	
147				440						445						450	
149	ctg	aag	aga	gtc	aag	tca	gag	gca	gta	act	gcc	cgc	cgt	gag	ccc	aga	1507
150	Leu	Lys	Arg	Val	Lys	Ser	Glu	Ala	Val	Thr	Ala	Arg	Arg	Glu	Pro	Arg	
151			455						460							465	
153	gaa	gag	gtg	gag	gat	gta	agc	agc	tat	ctc	tgt	aca	gaa	ttg	gac	aaa	1555
154	Glu	Glu	Val	Glu	Asp	Val	Ser	Ser	Tyr	Leu	Cys	Thr	Glu	Leu	Asp	Lys	
155			470						475							480	
157	atc	ccc	atg	gcc	cag	cgc	cga	cgc	ttc	aca	cgg	gtg	gag	atg	gcc	cga	1603
158	Ile	Pro	Met	Ala	Gln	Arg	Arg	Arg	Phe	Thr	Arg	Val	Glu	Met	Ala	Arg	
159			485						490							495	
161	gtg	ctc	atg	gaa	cgc	aac	cag	tac	aag	gaa	cgc	ctc	atg	gag	ctg	cag	1651
162	Val	Leu	Met	Glu	Arg	Asn	Gln	Tyr	Lys	Glu	Arg	Leu	Met	Glu	Leu	Gln	
163	500					505					510					515	
165	gag	gct	gtg	agg	tgg	act	gaa	atg	atc	aga	gca	tca	agg	gaa	cac	cca	1699
166	Glu	Ala	Val	Arg	Trp	Thr	Glu	Met	Ile	Arg	Ala	Ser	Arg	Glu	His	Pro	
167				520							525					530	
169	tct	gtc	cag	gag	aag	aag	aag	tcc	acc	atc	tgg	cag	ttc	ttt	agt	cgc	1747
170	Ser	Val	Gln	Glu	Lys	Lys	Lys	Ser	Thr	Ile	Trp	Gln	Phe	Phe	Ser	Arg	
171			535						540							545	
173	ctc	ttc	agc	tcc	tca	tct	agc	ccc	cct	ccg	gcc	aaa	cga	tcc	tac	cca	1795
174	Leu	Phe	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Ala	Lys	Arg	Ser	Tyr	Pro	
175			550						555							560	
177	tct	gtg	aac	att	cac	tac	aag	tca	ccc	act	gca	gct	ggc	ttt	agc	cag	1843
178	Ser	Val	Asn	Ile	His	Tyr	Lys	Ser	Pro	Thr	Ala	Ala	Gly	Phe	Ser	Gln	
179			565						570							575	
181	cgt	cgc	agc	cat	gct	ttg	tgc	cag	atc	tca	gcc	ggc	agc	agg	ccc	ctg	1891
182	Arg	Arg	Ser	His	Ala	Leu	Cys	Gln	Ile	Ser	Ala	Gly	Ser	Arg	Pro	Leu	
183	580					585					590					595	
185	gag	ttc	ttc	cct	gat	gat	gac	tgc	acc	tct	tct	gcc	cgg	cgg	gag	cag	1939
186	Glu	Phe	Phe	Pro	Asp	Asp	Asp	Cys	Thr	Ser	Ser	Ala	Arg	Arg	Glu	Gln	
187				600							605					610	
189	aag	cgg	gag	cag	tac	cgc	cag	gtt	cgt	gaa	cac	gtg	cgc	aat	gat	gac	1987
190	Lys	Arg	Glu	Gln	Tyr	Arg	Gln	Val	Arg	Glu	His	Val	Arg	Asn	Asp	Asp	
191				615							620					625	
193	ggg	agg	ctg	cag	gcc	tgt	ggg	tgg	agc	ctg	cct	gcc	aag	tac	aag	cag	2035

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194	Gly	Arg	Leu	Gln	Ala	Cys	Gly	Trp	Ser	Leu	Pro	Ala	Lys	Tyr	Lys	Gln	
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197	ctg	agc	ccc	aat	gga	ggc	cag	gaa	gac	acc	cgg	atg	aaa	aat	gtg	cct	2083
198	Leu	Ser	Pro	Asn	Gly	Gly	Gln	Glu	Asp	Thr	Arg	Met	Lys	Asn	Val	Pro	
199			645					650					655				
201	gtc	cct	gtg	tac	tgt	cgc	cct	ctg	gtg	gag	aag	gac	cct	tcg	aca	aag	2131
202	Val	Pro	Val	Tyr	Cys	Arg	Pro	Leu	Val	Glu	Lys	Asp	Pro	Ser	Thr	Lys	
203	660						665					670				675	
205	ctg	tgg	tgt	gct	gct	ggg	gtc	aac	ctg	agt	ggg	tgg	aag	cca	cat	gaa	2179
206	Leu	Trp	Cys	Ala	Ala	Gly	Val	Asn	Leu	Ser	Gly	Trp	Lys	Pro	His	Glu	
207						680					685					690	
209	gag	gac	tct	agc	aat	gga	ccc	aag	cct	gta	cca	ggg	cga	gac	cct	ctg	2227
210	Glu	Asp	Ser	Ser	Asn	Gly	Pro	Lys	Pro	Val	Pro	Gly	Arg	Asp	Pro	Leu	
211						695				700					705		
213	acc	tgt	gac	cgg	gaa	gga	gaa	ggc	gaa	ccc	aag	agc	aca	cac	cca	tca	2275
214	Thr	Cys	Asp	Arg	Glu	Gly	Glu	Gly	Glu	Pro	Lys	Ser	Thr	His	Pro	Ser	
215			710					715					720				
217	cct	gag	aag	aag	aag	gca	aag	gaa	acc	cct	gag	gca	gat	gct	acc	tcc	2323
218	Pro	Glu	Lys	Lys	Lys	Ala	Lys	Glu	Thr	Pro	Glu	Ala	Asp	Ala	Thr	Ser	
219			725					730					735				
221	agt	cgg	gta	tgg	atc	ctc	acc	agc	acc	ctg	aca	acc	agc	aag	gtg	gtg	2371
222	Ser	Arg	Val	Trp	Ile	Leu	Thr	Ser	Thr	Leu	Thr	Thr	Ser	Lys	Val	Val	
223	740					745					750					755	
225	atc	att	gat	gcc	aac	cag	cca	ggc	aca	att	gtg	gat	cag	ttc	aca	gtc	2419
226	Ile	Ile	Asp	Ala	Asn	Gln	Pro	Gly	Thr	Ile	Val	Asp	Gln	Phe	Thr	Val	
227						760					765					770	
229	tgc	aat	gcc	cac	gtc	ctg	tgt	atc	tcc	agc	att	cct	gcg	gcc	agt	gac	2467
230	Cys	Asn	Ala	His	Val	Leu	Cys	Ile	Ser	Ser	Ile	Pro	Ala	Ala	Ser	Asp	
231						775				780					785		
233	agt	gac	tat	ccc	cct	ggg	gag	atg	ttc	cta	gac	agt	gat	gtg	aac	cct	2515
234	Ser	Asp	Tyr	Pro	Pro	Gly	Glu	Met	Phe	Leu	Asp	Ser	Asp	Val	Asn	Pro	
235			790					795					800				
237	gaa	gat	tca	ggg	gct	gat	ggg	gtg	ctg	gct	ggc	atc	acc	ctg	gtg	ggg	2563
238	Glu	Asp	Ser	Gly	Ala	Asp	Gly	Val	Leu	Ala	Gly	Ile	Thr	Leu	Val	Gly	
239			805					810				815					
241	tgt	gct	acc	cgc	tgc	aat	gtt	cca	cgt	agc	aac	tgt	tcc	tca	cga	gga	2611
242	Cys	Ala	Thr	Arg	Cys	Asn	Val	Pro	Arg	Ser	Asn	Cys	Ser	Ser	Arg	Gly	
243	820					825					830					835	
245	gac	acc	cca	gta	ctg	gac	aag	ggg	cag	ggg	gat	gtg	gcg	acc	act	gcc	2659
246	Asp	Thr	Pro	Val	Leu	Asp	Lys	Gly	Gln	Gly	Asp	Val	Ala	Thr	Thr	Ala	
247						840					845					850	
249	aat	ggg	aag	gtc	aac	ccg	tcc	caa	tcc	aca	gaa	gaa	gcc	aca	gaa	gcc	2707
250	Asn	Gly	Lys	Val	Asn	Pro	Ser	Gln	Ser	Thr	Glu	Glu	Ala	Thr	Glu	Ala	
251						855					860					865	
253	aca	gag	gtg	cca	gac	cct	ggg	ccc	agc	gag	tca	gaa	gca	acg	aca	gtc	2755
254	Thr	Glu	Val	Pro	Asp	Pro	Gly	Pro	Ser	Glu	Ser	Glu	Ala	Thr	Thr	Val	
255						870					875					880	
257	cgg	ccc	ggg	cct	ctc	aca	gag	cat	gtc	ttt	act	gac	cca	gca	ccc	acc	2803
258	Arg	Pro	Gly	Pro	Leu	Thr	Glu	His	Val	Phe	Thr	Asp	Pro	Ala	Pro	Thr	

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259	885	890	895	
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263	900 905 910 915			
265	ggc acc att gta cag cct cag gtg gag ccc agt ggg gaa ctc tca aca	2899		
266	Gly Thr Ile Val Gln Pro Gln Val Glu Pro Ser Gly Glu Leu Ser Thr			
267	920 925 930			
269	aca acc agt agc gct gca ccc act atg tgg cta gga gcc cag aat ggc	2947		
270	Thr Thr Ser Ser Ala Ala Pro Thr Met Trp Leu Gly Ala Gln Asn Gly			
271	935 940 945			
273	tgg ctc tat gtg cat tca gcg gta gcc aac tgg aag aag tgt ctg cac	2995		
274	Trp Leu Tyr Val His Ser Ala Val Ala Asn Trp Lys Lys Cys Leu His			
275	950 955 960			
277	tcc atc aag cta aaa gac tct gtg ctg agc ctg gtg cat gtc aaa ggc	3043		
278	Ser Ile Lys Leu Lys Asp Ser Val Leu Ser Leu Val His Val Lys Gly			
279	965 970 975			
281	cga gtg ctg gta gct ctt gca gat ggg acc ctg gct atc ttc cat cgt	3091		
282	Arg Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile Phe His Arg			
283	980 985 990 995			
285	gga gag gat ggc cag tgg gac ctg agc aac tac cac cta atg gac ctg	3139		
286	Gly Glu Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu Met Asp Leu			
287	1000 1005 1010			
289	ggc cac cca cac cac tcc atc cgc tgc atg gct gtt gtg aat gac cga	3187		
290	Gly His Pro His His Ser Ile Arg Cys Met Ala Val Val Asn Asp Arg			
291	1015 1020 1025			
293	gtt tgg tgt ggc tac aag aac aag gtg cat gtt atc cag ccc aag aca	3235		
294	Val Trp Cys Gly Tyr Lys Asn Lys Val His Val Ile Gln Pro Lys Thr			
295	1030 1035 1040			
297	atg cag att gag aaa tca ttt gat gcc cac cca agg cgg gaa agc cag	3283		
298	Met Gln Ile Glu Lys Ser Phe Asp Ala His Pro Arg Arg Glu Ser Gln			
299	1045 1050 1055			
301	gta cgt cag ctg gcc tgg atc ggt gat gga gtg tgg gtc tct att cgc	3331		
302	Val Arg Gln Leu Ala Trp Ile Gly Asp Gly Val Trp Val Ser Ile Arg			
303	1060 1065 1070 1075			
305	ttg gat tct acc ctt cgg ctc tac cat gct cac acc cac cag cac ctg	3379		
306	Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr His Gln His Leu			
307	1080 1085 1090			
309	cag gat gtg gac att gag ccc tat gtt agc aag atg cta gga acc ggc	3427		
310	Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu Gly Thr Gly			
311	1095 1100 1105			
313	aag ctg ggc ttc tcc ttc gtg cgc atc aca gcc tta ctc att gca ggc	3475		
314	Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Leu Ile Ala Gly			
315	1110 1115 1120			
317	aac cgt ctg tgg gtg ggc act ggc aat ggg gtt gtc atc tcc atc ccc	3523		
318	Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Val Ile Ser Ile Pro			
319	1125 1130 1135			
321	ttg act gag act gtg gtc ctg cat cga ggc cag ctc cta ggg ctc cga	3571		
322	Leu Thr Glu Thr Val Val Leu His Arg Gly Gln Leu Leu Gly Leu Arg			
323	1140 1145 1150 1155			

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